IN THE SPECIFICATION

Please delete the paragraph beginning at page 10, line 3, with the following paragraph.

--The nucleotide sequence of ISRE from 441st to 456th position of the Sequence ID NO. 2 is ~~[GGTTCGTTTCTGCTC]~~ [GGTTTCGTTTCTGCGC] (Sequence ID No. 6). The 15th position of ISRE (corresponding to 455th position of Sequence ID No. 1) is guanine. Note that accordig to the ordinary representation in which the transcription initiation site is referred to as +1st position, 455th position is Sequence ID No. 1 is designated as -88th position.--

IN THE CLAIMS

--18. (Amended) A polynucleotide suitable for predicting the efficacy of interferon therapy using interferon-α and/or interferon-β for treating an individual who suffers from hepatitis C virus, comprising a polynucleotide selected from the group consisting of:

(at) the polynucleotide ~~of~~ comprising Sequence ID No. 1 ~~in the sequence listing~~;

(bt) ~~a modified polynucleotide derived from (at) by inclusion of one or several deletions, substitutions or additions at positions except for the 455th position~~ a polynucleotide having a nucleic acid sequence that is at least 99.83% identical to Sequence ID No. 1 and having MxA gene promoter activity;

~~(ct) a polynucleotide containing the sequence which spans from the 441st to the 455th position of Sequence ID No. 1;~~

~~(dt) a polynucleotide containing the sequence which spans from the 449th to the 459th position of Sequence ID No. 1;~~ and

(et) a complementary strand of the polynucleotide selected from the group consisting of (at)~~, (bt), (ct)~~ and (dt).

19. (Previously presented) The polynucleotide of Claim 18, which comprises (at).

20. (Previously presented) The polynucleotide of Claim 18, which comprises (bt).

21. (Canceled)

22. (Canceled)

23. (Previously presented) The polynucleotide of Claim 18, which comprises (et).

24. (Currently amended) The polynucleotide of Claim 18, further comprising at least one additional polynucleotide connected to said polynucleotide, the additional polynucleotide being selected from the group consisting of a promoter, an enhancer, an upstream activation sequence, a silencers, a upstream suppression sequence, an attenuator, a poly A tail, a nucleus transport signal, Kozak sequence, ISRE, a drug resistance factor, a gene of signal peptide, a gene of transmembrane ~~domein~~ domain, a gene of marker protein, a gene of interferon-responding protein, and a gene of interferon-non-responding protein.

25. (Previously presented) A polynucleotide suitable for predicting the efficacy of interferon therapy using interferon-α and/or interferon-β for treating an individual who suffers from hepatitis C virus, comprising a polynucleotide selected from the group consisting of:

(ag) the polynucleotide of Sequence ID No. 2 in the sequence listing;

(bg) a modified polynucleotide derived from (ag) by inclusion of one or several deletions, substitutions or additions at positions except for the 455th position;

(cg) a polynucleotide containing the sequence which spans from the 441st to the 455th position of Sequence ID No. 2;

(dg) a polynucleotide containing the sequence which spans from the 449th to the 459th position of Sequence ID No. 2; and

(eg) a complementary strand of the poly nucleotide selected from the group consisting of (ag), (bg), (cg) and (dg).

26. (Previously presented) The polynucleotide of Claim 25, which comprises (ag).

27. (Previously presented) The polynucleotide of Claim 25, which comprises (bg).

28. (Previously presented) The polynucleotide of Claim 25, which comprises (cg).

29. (Previously presented) The polynucleotide of Claim 25, which comprises (dg).

30. (Previously presented) The polynucleotide of Claim 25, which comprises (eg).

31. (Previously presented) The polynucleotide of Claim 25, further comprising at least one additional polynucleotide connected to said polynucleotide, the additional polynucleotide being selected from the group consisting of a promoter, an enhancer, an upstream activation sequence, a silencers, a upstream suppression sequence, an attenuator, a poly A tail, a nucleus transport signal, Kozak sequence, ISRE, a drug resistance factor, a gene of signal peptide, a gene of transmembrane domein, a gene of marker protein, a gene of interferon-responding protein, and a gene of interferon-non-responding protein.

32. (Previously presented) A polynucleotide suitable for predicting the efficacy of interferon therapy using interferon-α and/or interferon-β for treating an individual who suffers from hepatitis C virus, comprising a polynucleotide selected from the group consisting of:

(aa) the polynucleotide of Sequence ID No. 3 in the sequence listing;

(ba) a modified polynucleotide derived from (aa) by inclusion of one or several deletions, substitutions or additions at positions except for the 455th position;

(ca) a polynucleotide containing the sequence which spans from the 441st to the 455th position of Sequence ID No. 3;

(da) a polynucleotide containing the sequence which spans from the 449th to the 459th position of Sequence ID No. 3; and

(ea) a complementary strand of the polynucleotide selected from the group consisting of (aa), (ba), (ca) and (da).

33. (Previously presented) The polynucleotide of Claim 32, which comprises (aa).

34. (Previously presented) The polynucleotide of Claim 32, which comprises (ba).

35. (Previously presented) The polynucleotide of Claim 32, which comprises (ca).

36. (Previously presented) The polynucleotide of Claim 32, which comprises (da).

37. (Previously presented) The polynucleotide of Claim 32, which comprises (ea).

38. (Previously presented) The polynucleotide of Claim 32, further comprising at least one additional polynucleotide connected to said polynucleotide, the additional polynucleotide being selected from the group consisting of a promoter, an enhancer, an upstream activation sequence, a silencers, a upstream suppression sequence, an attenuator, a poly A tail, a nucleus transport signal, Kozak sequence, ISRE, a drug resistance factor, a gene of signal peptide, a gene of transmembrane domein, a gene of marker protein, a gene of interferon-responding protein, and a gene of interferon-non-responding protein.

39. (Previously presented) A polynucleotide suitable for predicting the efficacy of

interferon therapy using interferon-α and/or interferon-β for treating an individual who suffers from hepatitis C virus, comprising a polynucleotide selected from the group consisting of:

(ac) the polynucleotide of Sequence ID No. 4 in the sequence listing;

(bc) a modified polynucleotide derived from (ac) by inclusion of one or several deletions, substitutions or additions at positions except for the 455th position;

(cc) a polynucleotide containing the sequence which spans from the 441st to the 455th position of Sequence ID No. 4;

(dc) a polynucleotide containing the sequence which spans from the 449th to the 459th position of Sequence ID No. 4; and

(ec) a complementary strand of the polynucleotide selected from the group consisting of (ac), (bc), (cc) and (dc) mentioned above.

40. (Previously presented) The polynucleotide of Claim 39, which comprises (ac).

41. (Previously presented) The polynucleotide of Claim 39, which comprises (bc).

42. (Previously presented) The polynucleotide of Claim 39, which comprises (cc).

43. (Previously presented) The polynucleotide of Claim 39, which comprises (dc).

44. (Previously presented) The polynucleotide of Claim 39, which comprises (ec).

45. (Previously presented) The polynucleotide of Claim 39, further comprising at least one additional polynucleotide connected to said polynucleotide, the additional

polynucleotide being selected from the group consisting of a promoter, an enhancer, an upstream activation sequence, a silencers, a upstream suppression sequence, an attenuator, a poly A tail, a nucleus transport signal, Kozak sequence, ISRE, a drug resistance factor, a gene of signal peptide, a gene of transmembrane domein, a gene of marker protein, a gene of interferon-responding protein, and a gene of interferon-non-responding protein.

46. (Previously presented) A vector comprising the polynucleotide of Claim 18.

47. (Previously presented) A vector comprising the polynucleotide of Claim 25.

48. (Previously presented) A vector comprising the polynucleotide of Claim 32.

49. (Previously presented) A vector comprising the polynucleotide of Claim 39.

50. (Previously presented) A method for predicting the efficacy of interferon therapy using interferon-α and/or interferon-β for treating an individual who suffers from hepatitis C virus, comprising:

1) taking a sample containing a polynucleotide which includes at least one interferon-stimulated response element from the individual; and

2) determining whether the sample contains the polynucleotide of Claim 18, and

3a) predicting that the interferon therapy will be successful for said individual if the sample contains the polynucleotide of Claim 18 or

3b) predicting that the interferon therapy will not be successful for said individual if the sample does not contain the polynucleotide of Claim 18.

51. (Previously presented) A method for predicting the efficacy of interferon therapy using interferon-α and/or interferon-β for treating an individual who suffers from hepatitis C virus, comprising:

1) taking a sample containing a polynucleotide which includes at least one interferon-stimulated response element from the individual; and

2) determining whether the sample contains the polynucleotide of Claim 25, and

3a) predicting that the interferon therapy will be successful for said individual if the sample contains the polynucleotide of Claim 25 or

3b) predicting that the interferon therapy will not be successful for said individual if the sample does not contain the polynucleotide of Claim 25.

52. (Previously presented) A method for predicting the efficacy of interferon therapy using interferon-α and/or interferon-β for treating an individual who suffers from hepatitis C virus, comprising:

1) taking a sample containing a polynucleotide which includes at least one interferon-stimulated response element from the individual; and

2) determining whether the sample contains the polynucleotide of Claim 32, and

3a) predicting that the interferon therapy will be successful for said individual if the sample contains the polynucleotide of Claim 32 or

3b) predicting that the interferon therapy will not be successful for said individual if the sample does not contain the polynucleotide of Claim 32.

53. (Previously presented) A method for predicting the efficacy of interferon therapy using interferon-α and/or interferon-β for treating an individual who suffers from

hepatitis C virus, comprising:

1) taking a sample containing a polynucleotide which includes at least one interferon-stimulated response element from the individual; and

2) determining whether the sample contains the polynucleotide of Claim 39, and

3a) predicting that the interferon therapy will be successful for said individual if the sample contains the polynucleotide of Claim 39 or

3b) predicting that the interferon therapy will not be successful for said individual if the sample does not contain the polynucleotide of Claim 39.

54. (Previously presented) A method for rendering an interferon-insensitive individual to be interferon-sensitive, which comprises introducing the polynucleotide of Claim 18 into the interferon-insensitive individual.

55. (Previously presented) A method for rendering an interferon-insensitive individual to be interferon-sensitive, which comprises introducing the polynucleotide of Claim 25 into the interferon-insensitive individual.

56. (Previously presented) A method for rendering an interferon-insensitive individual to be interferon-sensitive, which comprises introducing the polynucleotide of Claim 32 into the interferon-insensitive individual.

57. (Previously presented) A method for rendering an interferon-insensitive individual to be interferon-sensitive, which comprises introducing the polynucleotide of Claim 39 into the interferon-insensitive individual.

58. (Previously presented) A non-human transgenic animal, into which has been introduced the polynucleotide of Claim 18.

59. (Previously presented) A non-human transgenic animal, into which has been introduced the polynucleotide of Claim 25.

60. (Previously presented) A non-human transgenic animal, into which has been introduced the polynucleotide of Claim 32.

61. (Previously presented) A non-human transgenic animal, into which has been introduced the polynucleotide of Claim 39.--

REMARKS

Claim 18 is amended. Claims 21 and 22 are cancelled without prejudice. Claims 18-20 and 23-61 are active in this application. Favorable reconsideration is respectfully requested.

At the outset, Applicants thank Examiner Chakrabart for the helpful comments during the courteous discussion of the present application held on July 31, 2003, which is summarized and expanded upon below. Further, Applicants thank Examiner Chakrabart for indicating that the amendments above, combined with the Sequence Alignment and Remarks below would further favorable prosecution of the present invention.

The rejections of the claims under 35 U.S.C. §112, first paragraph, are believed to be obviated by the amendments submitted above. The claims have been to remove the phrase "modified polynucleotide derived from (at) by inclusion of one or several deletions, substitutions or additions at positions except for the 455th position." Accordingly, withdrawal of this ground of rejection is respectfully requested.

It should be noted that Claim 18 is amended to include the phrase -- a polynucleotide having a nucleic acid sequence that is at least 99.83% identical to Sequence ID No. 1 and having MxA gene promoter activity--. This embodiment is clearly supported by the originally filed specification at SEQ ID NOS: 1-4. More specifically, the Sequence Alignment of SEQ ID NOS: 1-4 attached hereto clearly demonstrate the claimed homology rounded to the nearest hundredth of a percentage point. Further, these sequences are fully disclosed to have MxA gene promoter activity throughout the specification. Therefore, no new matter is believed to be introduced by the above-mentioned amendment.

The rejections of the claims under under 35 U.S.C. §102 over Krol et al. and/or Cross

et al. are believed to be obviated by the amendments submitted above. More specifically, the phrases "(ct) a polynucleotide containing the sequence which spans from the 441st to the 455th position of Sequence ID No. 1; (dt) a polynucleotide containing the sequence which spans from the 449th to the 459th position of Sequence ID No. 1" have been removed from the claims. The Office relies on Krol et al. and/or Cross et al. to demonstrate that either "(ct) a polynucleotide containing the sequence which spans from the 441st to the 455th position of Sequence ID No. 1" and/or "(dt) a polynucleotide containing the sequence which spans from the 449th to the 459th position of Sequence ID No. 1" may be disclosed by either Krol et al. and/or Cross et al.

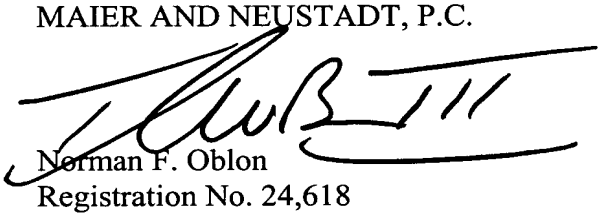
However, the Examiner indicated at the above-mentioned discussion that neither Krol et al. nor Cross et al. disclose or suggest a polynucleotide suitable for predicting the efficacy of interferon therapy using interferon-α and/or interferon-β for treating an individual who suffers from hepatitis C virus that may be either (at) a polynucleotide of having a Sequence ID No. 1 and/or (bt) a polynucleotide having a nucleic acid sequence that is at least 99.83% identical to Sequence ID No. 1 and having MxA gene promoter activity and/or a complementary strand of either of (at) and (dt).

In light of the above, neither Krol et al. nor Cross et al. disclose or suggest the claimed invention. Accordingly withdrawal of these grounds of rejection are respectfully requested.

Applicants respectfully submit that the present application is now in condition for allowance. Early notice to this effect is respectfully requested. Should anything further be required to place this application in condition for allowance, the Examiner is requested to contact the undersigned by telephone.

Respectfully submitted,

OBLON, SPIVAK, McCLELLAND,
MAIER AND NEUSTADT, P.C.



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